



11/31 #2 OIPE

## RAW SEQUENCE LISTING

DATE: 02/06/2002

PATENT APPLICATION: US/10/044,477

TIME: 16:19:38

Input Set : N:\Crf3\RULE60\10044477.raw

Output Set: N:\CRF3\02062002\J044477.raw

## SEQUENCE LISTING

## 1 (1) GENERAL INFORMATION:

2 (i) APPLICANT: Hillman, Jennifer L.  
3 Corley, Neil C.  
4 Shah, Purvi

ENTERED

5 (ii) TITLE OF INVENTION: HUMAN CORNICHON PROTEIN

6 (iii) NUMBER OF SEQUENCES: 3

7 (iv) CORRESPONDENCE ADDRESS:

8 (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.

9 (B) STREET: 3174 Porter Drive

10 (C) CITY: Palo Alto

11 (D) STATE: CA

12 (E) COUNTRY: USA

13 (F) ZIP: 94304

14 (v) COMPUTER READABLE FORM:

15 (A) MEDIUM TYPE: Diskette

16 (B) COMPUTER: IBM Compatible

17 (C) OPERATING SYSTEM: DOS

18 (D) SOFTWARE: FastSEQ for Windows Version 2.0

20 (vi) CURRENT APPLICATION DATA:

C--&gt; 21 (A) APPLICATION NUMBER: US/10/044,477

C--&gt; 22 (B) FILING DATE: 10-Jan-2002

24 (vii) PRIOR APPLICATION DATA:

26 (A) APPLICATION NUMBER: US/09/365,705

27 (B) FILING DATE: 02-Aug-1999

30 (A) APPLICATION NUMBER: US/08/950,168

31 (B) FILING DATE: 14-OCT-1997

33 (viii) ATTORNEY/AGENT INFORMATION:

34 (A) NAME: Billings, Lucy J.

35 (B) REGISTRATION NUMBER: 36,749

36 (C) REFERENCE/DOCKET NUMBER: PF-0401 US

37 (ix) TELECOMMUNICATION INFORMATION:

38 (A) TELEPHONE: 650-855-0555

39 (B) TELEFAX: 650-845-4166

40 (C) TELEX:

41 (2) INFORMATION FOR SEQ ID NO: 1:

42 (i) SEQUENCE CHARACTERISTICS:

43 (A) LENGTH: 144 amino acids

44 (B) TYPE: amino acid

45 (C) STRANDEDNESS: single

46 (D) TOPOLOGY: linear

47 (vii) IMMEDIATE SOURCE:

48 (A) LIBRARY: BLADNOT04

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49 (B) CLONE: 1318847

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

```

51 Met Ala Phe Thr Phe Ala Ala Phe Cys Tyr Met Leu Ala Leu Leu Leu
52 1 5 10 15
53 Thr Ala Ala Leu Ile Phe Phe Ala Ile Trp His Ile Ile Ala Phe Asp
54 20 25 30
55 Glu Leu Lys Thr Asp Tyr Lys Asn Pro Ile Asp Gln Cys Asn Thr Leu
56 35 40 45
57 Asn Pro Leu Val Leu Pro Glu Tyr Leu Ile His Ala Phe Phe Cys Val
58 50 55 60
59 Met Phe Leu Cys Ala Ala Glu Trp Leu Thr Leu Gly Leu Asn Met Pro
60 65 70 75 80
61 Leu Leu Ala Tyr His Ile Trp Arg Tyr Met Ser Arg Pro Val Met Ser
62 85 90 95
63 Gly Pro Gly Leu Tyr Asp Pro Thr Thr Ile Met Asn Ala Asp Ile Leu
64 100 105 110
65 Ala Tyr Cys Gln Lys Glu Gly Trp Cys Lys Leu Ala Phe Tyr Leu Leu
66 115 120 125
67 Ala Phe Phe Tyr Tyr Leu Tyr Gly Met Ile Tyr Val Leu Val Ser Ser
68 130 135 140

```

70 (2) INFORMATION FOR SEQ ID NO: 2:

71 (i) SEQUENCE CHARACTERISTICS:

72 (A) LENGTH: 1391 base pairs

73 (B) TYPE: nucleic acid

74 (C) STRANDEDNESS: single

75 (D) TOPOLOGY: linear

76 (vii) IMMEDIATE SOURCE:

77 (A) LIBRARY: BLADNOT04

78 (B) CLONE: 1318847

79 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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80 GTTTTACCCA GAGGGCCCTG CGACGCCTTT CTCCGCTGGC AACGGCGCCG CTCCCCGETC 60
81 CTCCTCCCCA GCCATGGCGT TCACGTTTCG GGCCTTCTGC TACATGCTGG CGCTGCTGCT 120
82 CACTGCCGCG CTCATCTTCT TCGCCATTG GCACATTATA GCATTTGATG AGCTGAAGAC 180
83 TGATTACAAG AATCCTATAG ACCAGTGTA TACCCTGAAT CCCCTGTGAC TCCCAGAGTA 240
84 CCTCATCCAC GCTTCTTCT GTGTCATGTT TCTTGTGCA GCAGAGTGGC TTACTACTGGG 300
85 TCTCAATATG CCCCTCTTGG CATATCATAT TTGGAGGTAT ATGAGTAGAC CAGTGATGAG 360
86 TGGCCAGGA CTCTATGACC CTACAACCAT CATGAATGCA GATATTCTAG CATATTGTCA 420
87 GAAGGAAGGA TGGTGCAAAT TAGCTTTTFA TCTTCTAGCA TTTTTTTACT ACCTATATGG 480
88 CATGATCTAT GTTTTGGTGA GCTCTTAGAA CAACACACAG AAGAATTGGT CCAGTTAAGT 540
89 GCATGCAAAA AGCCACCAAA TGAAGGGATT CTATCCAGCA AGATCCTGTC CAAGAGTAGC 600
90 CTGTGGAATC TGATCAGTTA CTTTAAAAAA TGAATCCTTA TTTTTTAAAT GTTCCACAT 660
91 TTTTGCTTGT GGAAAGACTG TTTTCATATG TTATACTCAG ATAAAGATTT TAAATGGTAT 720
92 TACGTATAAA TTAATATAAA ATGATTACCT CTGGTGTTGA CAGGTTTGAA CTTGCACTTC 780
93 TTAAGGAACA GCCATAATCC TCTGAATGAT GCATTAATTA CTGACTGTCC TAGTACATTG 840
94 GAAGCTTTTG TTTATAGGAA CTTGTAGGGC TCATTTTGGT TTCATTGAAA CAGTATCTAA 900
95 TTATAAATTA GCTGTAGATA TCAGGTGCTT CTGATGAAGT GAAAATGTAT ATCTGACTAG 960
96 TGGGAAACTT CATGGGTTTC CTCATCTGTC ATGTCGATGA TTATATATGG ATACATTTAC 1020
97 AAAAATAAAA AGCGGGAATT TTCCCTTCGC TTGAATATTA TCCCTGTATA TTGCATGAAT 1080
98 GAGAGATTC CATATTTCC ATCAGAGTAA TAAATATACT TGCTTTAATT CTTAAGCATA 1140

```

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```

99      AGTAAACATG ATATAAAAT ATATGCTGAA TTACTTGTGA AGAATGCATT TAAAGCTATT 1200
100     TTAAATGTGT TTTTATTTGT AAGACATTAC TTATTAAGAA ATTGGTTATT ATGCTTACTG 1260
101     TTCTAATCTG GTGGTAAAGG TATTCTTAAG AATTTCAGG TACTACAGAT TTTCAAAAC 1320
102     GAATGAGAGA AAATTGTATA ACCATCCTGC TGTTCCTTA GTGCAATACA ATAAAACTCT 1380
103     GAAATTAAAA A 1391

```

105 (2) INFORMATION FOR SEQ ID NO: 3:

106 (i) SEQUENCE CHARACTERISTICS:

107 (A) LENGTH: 144 amino acids

108 (B) TYPE: amino acid

109 (C) STRANDEDNESS: single

110 (D) TOPOLOGY: linear

111 (vii) IMMEDIATE SOURCE:

112 (A) LIBRARY: GenBank

113 (B) CLONE: 886769

114 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

```

115     Met Ala Phe Asn Phe Thr Ala Phe Thr Tyr Ile Val Ala Leu Ile Gly
116     1           5           10           15
117     Asp Ala Phe Leu Ile Phe Phe Ala Ile Phe His Val Ile Ala Phe Asp
118           20           25           30
119     Glu Leu Lys Thr Asp Tyr Lys Asn Pro Ile Asp Gln Cys Asn Ser Leu
120           35           40           45
121     Asn Pro Leu Val Leu Pro Glu Tyr Leu Leu His Ile Phe Leu Asn Leu
122           50           55           60
123     Leu Phe Leu Phe Cys Gly Glu Trp Phe Ser Leu Cys Ile Asn Ile Pro
124           65           70           75           80
125     Leu Ile Ala Tyr His Ile Trp Arg Tyr Lys Asn Arg Pro Val Met Ser
126           85           90           95
127     Gly Pro Gly Leu Tyr Asp Pro Thr Thr Val Leu Lys Thr Asp Thr Leu
128           100          105          110
129     Tyr Arg Asn Met Arg Glu Gly Trp Ile Lys Leu Ala Val Tyr Leu Ile
130           115          120          125
131     Ser Phe Phe Tyr Tyr Ile Tyr Gly Met Val Tyr Ser Leu Ile Ser Thr
132           130          135          140

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VERIFICATION SUMMARY

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L:21 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:22 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]